In the Claims:

Please cancel claims 1-20 without prejudice.

Please add new claims 29 – 61 as follows:

-- 29. A process for the preparation and improvement of a pantothenic acid-producing microorganism comprising amplifying a panE gene in said microorganism and then incubating said microorganism under conditions suitable for the production of the panE gene product, ketopantoate reductase.

30. The process of claim 29, wherein said panE gene is overexpressed in said microorganism.

31. The process of claim 29, wherein the endogenous panE gene is amplified.

32. The process of claim 29, wherein the ilvC gene is additionally amplified.

33. The process of claim 30, wherein overexpression is achieved by insertion of a gene encoding a protein having ketopantoate reductase activity into a plasmid vector and then transforming said microorganism with said plasmid vector.

34. The process of claim 33, wherein a promoter is incorporated upstream of said gene encoding a protein having ketopantoate activity.

35. The process of claim 30, wherein overexpression is achieved by mutating a promoter or other regulatory element upstream of a structural gene.

36. The process of claim 30, wherein overexpression is achieved by incorporating an expression cassette upstream of a structural gene.

37. The process of claim 29, wherein the gene that codes for ketopantoate reductase is amplified in a microorganism that has one or more metabolite resistance mutations.

38. The process of claim 29, wherein the gene which codes for ketopantoate reductase is amplified in a microorganism which has one or more antimetabolite resistance mutations.

39. The process of either claim 37 or claim 38, wherein said microorganism is resistant to one or more compounds selected from the group consisting of: the metabolite L-valine; the metabolite alpha-ketoisovaleric acid: the antimetabolite salicylic acid; the antimetabolite alpha-ketobutyric acid; beta-hydroxyaspartic acid; and the antimetabolite O-methylthreonine.

40. The process of claim 29, wherein said microorganism overexpresses at least one protein selected from the group consisting of: the protein having ketopantoate reductase activity encoded by the panE gene of *Escherichia coli*; the protein having ketopantoate reductase activity encoded by the ilvC gene of *Escherichia coli*; the protein having ketopantoate reductase activity encoded by the ilvC gene of *Corynebacterium glutamicum*; and the protein having ketopantoate reductase activity encoded by the YHR063c reading frame of *Saccharomyces cerevisiae*.

41. The process of claim 29, wherein, additionally, at least one gene of the metabolic path of pantothenic acid formation is amplified.

42. The process of claim 41, wherein said gene of the metabolic path of pantothenic acid formation is selected from the group consisting of: ketopantoate hydroxymethyltransferase (EC 4.1.2.12); aspartate 1-decarboxylase (EC 4.1.11); and pantothenate synthetase (EC 6.3.2.1).

43. The process of claim 42, wherein said microorganism is transformed with a plasmid vector comprising said gene.

44. The process of claim 29, wherein the activity of at least one gene in a metabolic pathway which reduces the formation of pantothenic acid is eliminated in said microorganism.

45. The process of claim 44, wherein the activity of the avtA gene is eliminated.

46. The process of claim 44, wherein the activity of the ilvE gene is eliminated.

47. The process of claim 29, wherein the ilvC gene of *C. glutamicum* is overexpressed or amplified in said microorganism.

48. The process of claim 29, wherein said microorganism is selected from the group consisting of: a Gram negative bacterium; a Gram positive bacterium; a fungus; and a yeast.

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49. The process of claim 48, wherein said microorganism is a bacterium of the genus Escherichia.

50. The process of claim 49, wherein said bacterium is of the species *Escherichia coli*.

51. The process of claim 48, wherein said microorganism is a bacterium of the genus Corynebacterium.

52. The process of claim 51, wherein said bacterium is of the species *Corynebacterium glutamicum*.

53. The process of claim 48, wherein said bacterium is a yeast of the genus Saccharomyces.

54. The process of claim 53, wherein said yeast of is the species *Saccharomyces cerevisiae*.

55. The process of claim 44, wherein said microorganism is *Escherichia coli* and the activity of either the avtA or ilvE gene is eliminated in said microorganism.

56. The plasmid vector pFE80 characterized by the restriction map shown in Figure 6 and deposited as *E. coli* K12 strain MG 1655/pFE80 under deposit number DSM 12414.

57. The plasmid vector pFE65, characterized by the restriction map shown in Figure 5 and deposited as *E. coli* K12 strain MG 1655/pFE65 under deposit number DSM 12382.

58. The plasmid vector pFE32, characterized by the restriction map shown in Figure 4 and deposited as *E. coli* K12 strain MG 1655/pFE32 under the deposit number DSM 12413.

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59. The process of claim 29, wherein K12 strain FE6 is used, said strain being deposited under deposit number DSM 12379.

60. The process of claim 29, wherein *E. coli* K12 strain FE7 is used, said strain being deposited under deposit number DSM 12380.

61. The microorganism produced by the process of claim 29. --